

ATTACHMENT A

<110> APPLICANT: Better, Marc D.  
Horwitz, Arnold H.  
<120> TITLE OF INVENTION: Human Engineered to Antibodies to Ep-CAM  
<130> FILE REFERENCE: 14923US02  
<140> CURRENT APPLICATION NUMBER: US/10/816,276  
<141> CURRENT FILING DATE: 2004-03-31  
<150> PRIOR APPLICATION NUMBER: 60/459,334  
<151> PRIOR FILING DATE: 2003-03-31  
<160> NUMBER OF SEQ ID NOS: 59  
<170> SOFTWARE: PatentIn version 3.2

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Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
80 85 90  
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Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Thr Lys  
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Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
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Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
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Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
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cct gga gag aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc	144	
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
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Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu		
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Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr GLY		
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Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser		
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act gcc aat ttg cag atc aac aac ctc aaa agt gag gac acg gct aca	336	
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tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga	384	
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly		
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Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro		
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Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp			864
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Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn			912
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Lys			

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Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
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Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
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Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro
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Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser
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Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala
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Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe
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Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
						80			85				90		
tgt	gct	cag	aac	cta	gag	ctt	cca	cg	acg	ttc	ggt	cag	ggc	acc	aag
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys
						95			100				105		
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
						110			115				120		
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
125						130				135				140	
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	aat
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
						145				150				155	
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
						160			165				170		
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
						175			180				185		
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
						190			195				200		
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag
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      -1   1           5           10
      Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
      15           20           25
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
      30           35           40
      Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
      45           50           55           60
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
      65           70           75
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      80           85           90
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
      95           100          105

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Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
110						115						120			
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
125					130				135					140	
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
					145				150				155		
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
					160			165				170			
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
					175			180				185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
					190			195			200				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
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	tgcagactgg gtcatcacga tgtct	85	
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	gcagaaaacca gggcagtctc ctcagctg	88	
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      atagatgagc agctgaggag actgcc                                86

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      gtaataaact cccac                                75

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<223> Low risk Primers Reverse Primer: KR ING-1 Light Chain Oligos
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Light Chain Oligos (Kappa Moderate)

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-15 -10 -5  
gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag 96  
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys  
-1 1 5 10  
cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc 144  
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
15 20 25  
aca aaa tat gga atg aac tgg gtg aag cag gct cca gga cag ggt tta 192  
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu  
30 35 40 45  
aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt 240  
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly  
50 55 60  
gat gac ttc aag gga cgg ttt acc ttc acc ttg gac acc tct act agc 288  
Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser  
65 70 75  
act gcc tat ttg gaa atc tct tct ctc cgg agt gag gac acg gct aca 336  
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr  
80 85 90  
tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga 384  
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly  
95 100 105  
acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc 432  
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
110 115 120 125  
ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg gcc ctg 480  
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
130 135 140  
ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg 528  
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
145 150 155  
aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta 576  
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

160	165	170		
cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc	acc gtg ccc tcc		624	
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser				
175	180	185		
agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc			672	
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro				
190	195	200	205	
agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa			720	
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys				
210	215	220		
act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg			768	
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro				
225	230	235		
tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc			816	
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser				
240	245	250		
cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac gaa gac			864	
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp				
255	260	265		
cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat			912	
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn				
270	275	280	285	
gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cggtg			960	
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val				
290	295	300		
gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag			1008	
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu				
305	310	315		
tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa			1056	
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys				
320	325	330		
acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc			1104	
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr				
335	340	345		
ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc			1152	
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr				
350	355	360	365	
tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag			1200	
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu				
370	375	380		
agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg			1248	
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu				
385	390	395		
gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg gac aag			1296	
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys				
400	405	410		
agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag			1344	
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu				
415	420	425		
gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt			1392	
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aaa tga			1398	
Lys				

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-1 1 5 10  
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
15 20 25  
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu  
30 35 40 45  
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly  
50 55 60  
Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser  
65 70 75  
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr  
80 85 90  
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly  
95 100 105  
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
110 115 120 125  
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
130 135 140  
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
145 150 155  
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
160 165 170  
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
175 180 185  
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
190 195 200 205  
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys  
210 215 220  
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
225 230 235  
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
240 245 250  
Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp  
255 260 265  
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
270 275 280 285  
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
290 295 300  
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
305 310 315  
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
320 325 330  
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
335 340 345  
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr  
350 355 360 365  
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
370 375 380  
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
385 390 395  
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
400 405 410

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
         415                               420                               425  
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
         430                               435                               440                               445  
 Lys

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Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser		
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agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc		672
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro		
190							195				200				205		
agc	aac	acc	aag	gtg	gac	aag	aga	gtt	gag	ccc	aaa	tct	tgt	gac	aaa		720
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys		
							210				215				220		
act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg		768
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro		
							225				230				235		
tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc		816
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser		
							240				245				250		
cg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtc	agc	cac	gaa	gac		864
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp		
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cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat		912
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn		
							270				275				280		285
gcc	aag	aca	aag	ccg	cg	gag	gag	cag	tac	aac	agc	acg	tac	cg	gt		960
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val		
							290				295				300		
gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	tgg	ctg	aat	ggc	aag	gag		1008	
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu		
							305				310				315		
tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa		1056
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys		
							320				325				330		
acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gt	tac	acc		1104
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr		
							335				340				345		
ctg	ccc	cca	tcc	cg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc		1152
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr		
							350				355				360		365
tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag		1200
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu		
							370				375				380		
agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg		1248
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu		
							385				390				395		
gac	tcc	gac	ggc	tcc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag		1296	
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys		
							400				405				410		
agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag		1344
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu		
							415				420				425		
gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt		1392
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly		
							430				435				440		445
aaa	tga																1398
Lys																	

<210> 21  
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<212> PRT  
<213> Homo Sapiens

<400> 21

Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser  
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-1 1 5 10  
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
15 20 25  
Thr Lys Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
30 35 40 45  
Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly  
50 55 60  
Gln Lys Phe Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser  
65 70 75  
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
80 85 90  
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly  
95 100 105  
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
110 115 120 125  
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
130 135 140  
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
145 150 155  
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
160 165 170  
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
175 180 185  
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
190 195 200 205  
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys  
210 215 220  
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
225 230 235  
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
240 245 250  
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
255 260 265  
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
270 275 280 285  
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
290 295 300  
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
305 310 315  
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
320 325 330  
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
335 340 345  
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr  
350 355 360 365  
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
370 375 380  
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
385 390 395  
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
400 405 410  
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
415 420 425

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
430 435 440 445  
Lys

<210> 22  
<211> 91  
<212> DNA  
<213> HomoSapiens  
<220>  
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<223> GL1 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos  
(gamma low)  
<400> 22  
tgtcgacacc atggcttggg tgtccacatt gctattcctg atggcagctg cccaaagtgc 60  
ccaagcacag atccagttgg tgcagtctgg a 91

<210> 23  
<211> 90  
<212> DNA  
<213> HomoSapiens  
<220>  
<221> misc\_feature  
<223> GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos  
(gamma low)  
<400> 23  
atattttgtg aaggttatatc cagaaggcatt gcaggagatc ttgacggact ctccaggctt 60  
cttcacacctca ggtccagact gcaccaactg 90

<210> 24  
<211> 91  
<212> DNA  
<213> HomoSapiens  
<220>  
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<223> GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos  
(gamma low)  
<400> 24  
tggatataacc ttcacaaaaat atggaatgaa ctgggtgaag caggctccag gacagggttt 60  
aaagtggatg ggctggataa acacctacac t 91

<210> 25  
<211> 90  
<212> DNA  
<213> HomoSapiens  
<220>  
<221> misc\_feature  
<223> GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos  
(gamma low)  
<400> 25  
cagtgttagt agaggtgtcc aaggtgaagg taaaaccgtcc cttgaagtca tcaccatatg 60  
ttggctttc agtgttaggtg tttatccagc 90

<210> 26  
<211> 90  
<212> DNA  
<213> HomoSapiens  
<220>

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<221> misc_feature
<223> GL5 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 26
      gacacctcta ctagcactgc statttggaa atcttttc tccggagtga ggacacggct      60
            acatatttct gtgcaagatt tggctctgct                         90

<210> 27
<211> 85
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 27
      gaccgatggg ccctttgtgc tggctgagga gacggtgacc aaggttcctt gaccccagta      60
            gtccacagca gagccaaatc ttgca                         85

<210> 28
<211> 22
<212> DNA
<213> HomoSapiens
<220>
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<223> Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers
      Forward primer:GF
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      ttatgtcgac accatggctt gg                                         22

<210> 29
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<212> DNA
<213> HomoSapiens
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<223> Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers
      -Reverse Primer GR
<220>
<221> misc_feature
<223> ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR
<400> 29
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<210> 30
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<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
      + Moderate Risk Primers
<400> 30
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            cttcacctca gctccagact gcaccaactg                         90

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<211> 91
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<220>
<221> misc_feature
<223> GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
      + Moderate Risk Primers
<400> 31
      tggatataacc ttcacaaaaat atggaatgaa ctgggtgcga caggctccag gacaaggttt      60
      agagtggatg ggctggataa acacctacac t                                91

<210> 32
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
      + Moderate Risk Primers
<400> 32
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      ttggctcttc agtgttagtg tttatccagc                                90

<210> 33
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
      + Moderate Risk Primers
<400> 33
      gacacctcta ctagcactgc ctatttgaa atctcttcgc tccggagtga ggacacggct      60
      gtgtatttct gtgcaagatt tggctctgct                                90

<210> 34
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<212> DNA
<213> Homo sapiens
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<220>
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      Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
      -20          -15           -10          -5
      gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca      96
      Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
      -1   1           5           10
      gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt      144

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Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser				
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ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa				192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys				
30	35	40		
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc				240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala				
45	50	55	60	
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc				288
Ser Gly Val Pro Asp Arg Phe Ser Ser Gly Ser Gly Thr Asp Phe				
65	70	75		
act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac				336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr				
80	85	90		
tgt gct cag aac cta gag ctt ccg cg agg ttc ggt cag ggc acc aag				384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys				
95	100	105		
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg				432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro				
110	115	120		
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg				480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu				
125	130	135	140	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat				528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp				
145	150	155		
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac				576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp				
160	165	170		
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa				624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys				
175	180	185		
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag				672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln				
190	195	200		
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag				720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys				
205	210	215		

<210> 35

<211> 239

<212> PRT

<213> Homo sapiens

<400> 35

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro			
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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro			
-1	1	5	10

Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser			
15	20	25	

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys			
30	35	40	

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala			
45	50	55	60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe			
65	70	75	

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
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80	85	90
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys		
95	100	105
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro		
110	115	120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu		
125	130	135
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp		
145	150	155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp		
160	165	170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys		
175	180	185
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln		
190	195	200
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
205	210	215

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<223> P2=P Human Engineered (low risk) ING1 light Chain with one  
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-20 -15 -10 -5	
gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca	96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro	
-1 1 5 10	
gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt	144
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser	
15 20 25	
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa	192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
30 35 40	
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aca aga gcc	240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
45 50 55 60	
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc	288
Ser Gly Val Pro Asp Arg Phe Ser Ser Gly Ser Gly Thr Asp Phe	
65 70 75	
act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac	336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag	384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
95 100 105	

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
175 180 185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
190 195 200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205 210 215	
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<b>&lt;211&gt;</b> 239	
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<b>&lt;213&gt;</b> Homo sapiens	
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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro	
-1 1 5 10	
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser	
15 20 25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
30 35 40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
45 50 55 60	
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	
65 70 75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
95 100 105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
175 180 185	
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
190 195 200	
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205 210 215	

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 <223> P3=P Human Engineered (low risk) ING1 light Chain with one  
       moderate risk proline change; proline at position 18 (P3)  
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-20								-15			-10				-5		
gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	gca	ctc	tcc	aat	cca		96
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro		
-1								1			5				10		
gtc	act	ctg	gga	gag	ccg	ggt	tcc	atc	tcc	tgc	cg	tct	agt	aag	agt		144
Val	Thr	Leu	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser		
15								20			25						
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa		192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Tyr	Tyr	Leu	Gln	Lys		
30								35			40						
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc		240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala		
45								50			55				60		
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc		288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe		
65								70			75						
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac		336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr		
80								85			90						
tgt	gct	cag	aac	cta	gag	ctt	ccg	cg	ac	ttc	gg	cc	acc	aag			384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys		
95								100			105						
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg		432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro		
110								115			120						
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg		480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu		
125								130			135				140		
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat		528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp		
145								145			150				155		
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac		576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp		
160								165			170						
agc	aag	gac	agc	acc	tac	agc	ctc	agc	acc	ctg	acg	ctg	agc	aaa		624	
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys		
175								180			185						
gca	gac	tac	gag	aaa	cac	aaa	gtc	gcc	tgc	gaa	gtc	acc	cat	cag		672	
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln		

190	195	200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag		Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	720
205	210	215	

<210> 39

<211> 239

<212> PRT

<213> Homo sapiens

<400> 39

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Trp Ile Pro			
-20	-15	-10	-5
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro			
-1 1	5	10	
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser			
15	20	25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys			
30	35	40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala			
45	50	55	60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe			
65	70	75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
80	85	90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys			
95	100	105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
110	115	120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
125	130	135	140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
145	150	155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
160	165	170	
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
175	180	185	
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
190	195	200	
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
205	210	215	

<210> 40

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<223> P1P2=Human Engineered (low risk) ING1 light Chain with one  
moderate risk proline change; proline at position 8 (P1) 15 (P2)

<220>

<221> CDS

<222> (1)..(717)

<220>

<221> mat\_peptide

<222> (61)..()

<400> 40

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Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro			
-20	-15	-10	-5
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca			96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro			
-1 1	5	10	
gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt			144
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser			
15	20	25	
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa			192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys			
30	35	40	
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc			240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala			
45	50	55	60
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc			288
Ser Gly Val Pro Asp Arg Phe Ser Ser Gly Ser Gly Thr Asp Phe			
65	70	75	
act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac			336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
80	85	90	
tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag			384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys			
95	100	105	
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg			432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
110	115	120	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg			480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
125	130	135	140
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat			528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
145	150	155	
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac			576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
160	165	170	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa			624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
175	180	185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag			672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
190	195	200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag			720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
205	210	215	

<210> 41

<211> 239

<212> PRT

<213> Homo sapiens

<400> 41

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro

-20 -15 -10 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro

-1 1 5 10

Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser

15 20 25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys

30	35	40
Pro	Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
45	50	55
Ser	Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	60
	65	70
Thr	Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	75
	80	85
Cys	Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	90
	95	100
Leu	Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	105
	110	115
Pro	Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	120
125	130	135
Leu	Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	140
	145	150
Asn	Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	155
	160	165
Ser	Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	170
	175	180
Ala	Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	185
	190	195
Gly	Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	200
205	210	215

<210> 42  
<211> 720  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> misc\_feature  
<223> P1P3= Human Engineered (low risk) ING1 light Chain with one  
moderate risk proline change; proline at position 8 (P1) 18 (P3)  
<220>  
<221> CDS  
<222> (1)..(717)  
<220>  
<221> mat\_peptide  
<222> (61)..()  
<400> 42

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-20 -15 -10 -5	
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca	96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro	
-1 1 5 10	
gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt	144
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser	
15 20 25	
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa	192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
30 35 40	
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aca aga gcc	240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
45 50 55 60	
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc	288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	
65 70 75	

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac	336		
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
80	85	90	
tgt gct cag aac cta gag ctt ccg cg <sup>g</sup> acg ttc ggt cag ggc acc aag	384		
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys			
95	100	105	
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	432		
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
110	115	120	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	480		
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
125	130	135	140
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	528		
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
145	150	155	
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac	576		
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
160	165	170	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa	624		
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
175	180	185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag	672		
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
190	195	200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag	720		
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
205	210	215	

<210> 43

<211> 239

<212> PRT

<213> Homo sapiens

<400> 43

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro			
-20	-15	-10	-5
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro			
-1	1	5	10
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser			
15	20	25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys			
30	35	40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala			
45	50	55	60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe			
65	70	75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
80	85	90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys			
95	100	105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
110	115	120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
125	130	135	140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
145	150	155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
160	165	170	

Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
175							180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
190						195					200				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
205							210				215				

<210> 44

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<223> P2P3=Human Engineered (low risk) ING1 light Chain with one  
moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>

<221> CDS

<222> (1)..(717)

<220>

<221> mat\_peptide

<222> (61)..()

<400> 44

atg	agg	ttc	tct	gct	cag	ctt	ctg	ggg	ctg	ctt	gtg	ctc	tgg	atc	cct	48
Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro	
-20						-15				-10					-5	
gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	gca	ctc	tcc	aat	cca	96
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro	
-1	1					5								10		
gtc	act	cct	gga	gag	ccg	ggg	tcc	atc	tcc	tgc	cg	tct	agt	aag	agt	144
Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
15							20				25					
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
30						35					40					
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45						50				55			60			
tca	ggg	gtc	cca	gac	agg	tcc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe		
65							70					75				
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
80						85					90					
tgt	gct	cag	aac	cta	gag	ctt	ccg	cg	acg	tcc	gg	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
95						100					105					
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
110						115					120					
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
125						130				135			140			
ctg	aat	aac	tcc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
145							150				155					
aac	gcc	ctc	caa	tgc	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	

160	165	170	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa			624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
175	180	185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag			672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
190	195	200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag			720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
205	210	215	
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<211> 239			
<212> PRT			
<213> Homo sapiens			
<400> 45			
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro			
-20	-15	-10	-5
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro			
-1	1	5	10
Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser			
15	20	25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys			
30	35	40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala			
45	50	55	60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe			
65	70	75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Asp Val Gly Val Tyr Tyr			
80	85	90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys			
95	100	105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
110	115	120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
125	130	135	140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
145	150	155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
160	165	170	
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
175	180	185	
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
190	195	200	
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
205	210	215	
<210> 46			
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<212> DNA			
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<223> P1 Oligo Human Engineered ING-1 with proline oligos			
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actcttacta gaccggcagg agatgaaacc tgactctccc agagtgactg gattggagag	60		
tggagactgg gtcatcacga tgtct	85		

<210> 47  
<211> 85  
<212> DNA  
<213> Homo Sapiens  
<220>  
<221> misc\_feature  
<223> P2 Oligo Human Engineered ING-1 with proline oligos  
<400> 47  
actcttacta gaccggcagg agatggaacc tgactctcca ggagtgactg gattggagag 60  
tgcagactgg gtcatcacga tgtct 85

<210> 48  
<211> 85  
<212> DNA  
<213> Homo Sapiens  
<220>  
<221> misc\_feature  
<223> P3 Oligo Human Engineered ING-1 with proline oligos  
<400> 48  
actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60  
tgcagactgg gtcatcacga tgtct 85

<210> 49  
<211> 85  
<212> DNA  
<213> Homo Sapiens  
<220>  
<221> misc\_feature  
<223> P1P2 Oligo Human Engineered ING-1 with proline oligos  
<400> 49  
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag 60  
tgcagactgg gtcatcacga tgtct 85

<210> 50  
<211> 85  
<212> DNA  
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<220>  
<221> misc\_feature  
<223> P1P3 Oligo Human Engineered ING-1 with proline oligos  
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actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60  
tggagactgg gtcatcacga tgtct 85

<210> 51  
<211> 85  
<212> DNA  
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<220>  
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<223> P2P3 Oligo Human Engineered ING-1 with proline oligos  
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tgcagactgg gtcatcacga tgtct 85

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<221> misc_feature		
<223> Reverse Primer KBsr ING-1 Light Chain		
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Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala		
1                 5                 10                 15		
acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac		96
Thr Ala Thr Phe Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr		
20                 25                 30		
aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt		144
Lys Leu Ala Val Asn Cys Phe Val Asn Asn Arg Gln Cys Gln Cys		
35                 40                 45		
act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc		192
Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala		
50                 55                 60		
aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga		240
Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg		
65                 70                 75                 80		
aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat		288
Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp		
85                 90                 95		
cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc		336
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly		
100                 105                 110		
acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac		384
Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp		
115                 120                 125		
aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc		432
Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile		
130                 135                 140		
atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa		480
Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys		
145                 150                 155                 160		
agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg		528
Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu		
165                 170                 175		
gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act		576
Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr		
180                 185                 190		
att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac		624

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp			
195	200	205	
ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc			672
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser			
210	215	220	
ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg			720
Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu			
225	230	235	240
gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca			768
Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala			
245	250	255	
cct gaa ttc tca atg cag ggt cta aaa taa			798
Pro Glu Phe Ser Met Gln Gly Leu Lys			
260	265		

<210> 54

<211> 265

<212> PRT

<213> Homo sapiens

<400> 54

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala			
1	5	10	15
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr			
20	25	30	
Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys			
35	40	45	
Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala			
50	55	60	
Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg			
65	70	75	80
Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp			
85	90	95	
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly			
100	105	110	
Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp			
115	120	125	
Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile			
130	135	140	
Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys			
145	150	155	160
Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu			
165	170	175	
Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr			
180	185	190	
Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp			
195	200	205	
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser			
210	215	220	
Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu			
225	230	235	240
Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala			
245	250	255	
Pro Glu Phe Ser Met Gln Gly Leu Lys			
260	265		

<210> 55

<211> 945

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<212> DNA
<213> Homo sapiens
<220>
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Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
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Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
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Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
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Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
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Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
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